



RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

09/030,482

Art Unit / Team No. :

01PE

Date Processed by STIC:

3/7/98

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/030,482

DATE: 03/07/98
TIME: 13:53:51

INPUT SET: S2880.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply
Corrected Diskette Needed

1 SEQUENCE LISTING
2
3 (1) General Information:
4 (i) APPLICANT: Snutch, Terry P.
5 Baillie, David L.
6 (ii) TITLE OF INVENTION: Novel Human Calcium Channels and Related Probes, Cell Line
7 and Methods
8 (iii) NUMBER OF SEQUENCES: 20
9 (iv) CORRESPONDENCE ADDRESS:
10 (A) ADDRESSEE: Oppedahl & Larson
11 (B) STREET: 1992 Commerce Street Suite 309
12 (C) CITY: Yorktown
13 (D) STATE: NY
14 (E) COUNTRY: USA
15 (F) ZIP: 10598
16 (v) COMPUTER READABLE FORM:
17 (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
18 (B) COMPUTER: IBM Compatible
19 (C) OPERATING SYSTEM: MS DOS 6.0
20 (D) SOFTWARE: WordPerfect
21 (vi) CURRENT APPLICATION DATA:
22 (A) APPLICATION NUMBER:
23 (B) FILING DATE:
24 (C) CLASSIFICATION:
25 (viii) ATTORNEY/AGENT INFORMATION:
26 (A) NAME: Larson, Marina T.
27 (B) REGISTRATION NUMBER: 32038
28 (C) REFERENCE/DOCKET NUMBER: NMED.P-001-US
29 (ix) TELECOMMUNICATION INFORMATION:
30 (A) TELEPHONE: (914) 245-3252
31 (B) TELEFAX: (914) 962-4330
32

ERRORED SEQUENCES FOLLOW:

94 (2) INFORMATION FOR SEQ ID NO: 5:
95 (i) SEQUENCE CHARACTERISTICS:
96 (A) LENGTH: 24
97 (B) TYPE: nucleic acid
98 (C) STRANDEDNESS: single
99 (D) TOPOLOGY: linear
100 (ii) MOLECULE TYPE: other nucleic acid

(next page)

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101 (iii) HYPOTHETICAL: no
102 (iv) ANTI-SENSE: no
103 (vi) ORIGINAL SOURCE:
104 (A) ORGANISM: rat
105 (ix) FEATURE: oligonucleotide probe for locating calcium channel genes
106 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
--> 107 GTTAAATCCA ACGTCTTCTA CTGG
108

This goes UNDER
(IX) FEATURE:
(D) OTHER INFORMATION:

Edit all responses
to (IX) FEATURE:

267 (2) INFORMATION FOR SEQ ID NO: 16:
268 (i) SEQUENCE CHARACTERISTICS:
--> 269 (A) LENGTH: 123
270 (B) TYPE: nucleic acid
271 (C) STRANDEDNESS: single
272 (D) TOPOLOGY: linear
273 (ii) MOLECULE TYPE: other nucleic acid
274 (iii) HYPOTHETICAL: no
275 (iv) ANTI-SENSE: no
276 (vi) ORIGINAL SOURCE:
277 (A) ORGANISM: human
278 (ix) FEATURE: expressed sequence tag H55544 (D) OTHER INFORMATION: C
279 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
280 GTATCTCTGG TTACTTTAGT AGCCAACACT CTTGGCTACT CAGACCTTGG TCCCATTAAA 60
281 TCCCTGCGAA CTTGAGAGC ACTAAGACCT CTAAGAGCTT TGTCTAGATT TGAAGGAATG 120
282 AGG
283

123 ← insert

305 (2) INFORMATION FOR SEQ ID NO: 18:
306 (i) SEQUENCE CHARACTERISTICS:
307 (A) LENGTH: 5562
308 (B) TYPE: nucleic acid
309 (C) STRANDEDNESS: double
310 (D) TOPOLOGY: linear
311 (ii) MOLECULE TYPE: cDNA
312 (iii) HYPOTHETICAL: no
313 (iv) ANTI-SENSE: no
314 (vi) ORIGINAL SOURCE:
315 (A) ORGANISM: human
316 (ix) FEATURE: human alpha-I partial sequence from BAC bk206c7
317 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
318
319 ATG TTT TTC GTC TCA GCC AAT CCC TGG GTG AGT TTC ACC AGT TTT GAT TTA AAC 54
320 Met Phe Phe Val Ser Ala Asn Pro Trp Val Ser Phe Thr Ser Phe Asp Leu Asn *more there*
321 *on next line*
322
323 GTG GCC AAT ATG GAC AAC TTC TTC GCC CCC GTT TTC ACC ATG GGC AAA TAT TAT 108
324 Val Ala Asn Met Asp Asn Phe Phe Ala Pro Val Phe Thr Met Gly Lys Tyr Tyr
325
326
327 ACG CAA GGC GAC AAG GTG CTG ATG CCG CTG GCG ATT CAG GCT CTG AAA CAG CTG 162
328 Thr Gln Gly Asp Lys Val Leu Met Pro Leu Ala Ile Gln Ala Leu Lys Gln Leu
329
330

1) Per 1.822 (h) and (i) of Sequence Rules, only 16 amino acids and 16 triplets allowed per line;
2) Per 1.822 (m) of Sequence Rules, number all amino acids under every 5 amino acids. Please number all amino acids in the sequence listing.

RAW SEQUENCE LISTING PATENT APPLICATION US/09/030,482

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INPUT SET: S2880.raw

-->	331	ATG TTC AAA TTG GTG GCC ACT GTT GCT CGA ACA CAT GCT ACA CCG TCA CAC ATC	206
	332	Met Phe Lys Leu Val Ala Thr Val Ala Arg Thr His Ala Thr Pro Ser His Ile	216
	333		
	334		
-->	335	ACG GGT GGT CCT GGA ACA GGG ATG CAC ACG GGC ACC TTC CAG GAA GGA GCT GAG	270 OK
	336	Thr Gly Gly Pro Gly Thr Gly Met His Thr Gly Thr Phe Gln Glu Gly Ala Glu	
	337		
	338		
	339	CCT GGT TCA TCT CAG CAC CCT GAG GCA CAG GCC ACG TAT ACA GCA GGG TGC ACC	324
	340	Pro Gly Ser Ser Gln His Pro Glu Ala Gln Ala Thr Tyr Thr Ala Gly Cys Thr	
	341		
	342		
	343	CCA GCC CCC ACG GGC GAT CCC ACC TGC TGC TTT GTC CTT GAC TTG GTG TGC ACG	378
	344	Pro Ala Pro Thr Gly Asp Pro Thr Cys Cys Phe Val Leu Asp Leu Val Cys Thr	
	345		
	346		
	347	TGG TTT GAA TGT GTC AGC ATG CTG GTG ATC CTG CTG AAC TGC GTG ACA CTT GGC	432
	348	Trp Phe Glu Cys Val Ser Met Leu Val Ile Leu Leu Asn Cys Val Thr Leu Gly	
	349		
	350		
	351	ATG TAC CAG CCG TGC GAC GAC ATG GAC TGC CTG TCC GAC CGC TGC AAG ATC CTG	486
	352	Met Tyr Gln Pro Cys Asp Asp Met Asp Cys Leu Ser Asp Arg Cys Lys Ile Leu	
	353		
	354		
	355	CAG GTC TTT GAT GAC TTC ATC TTT ATC TTC TTT GCC ATG GAG ATG GTG CTC AAG	540
	356	Gln Val Phe Asp Asp Phe Ile Phe Ile Phe Phe Ala Met Glu Met Val Leu Lys	
	357		
	358		
	359	ATG GTG GCC CTG GGG ATT TTT GGC AAG AAG TGC TAC CTC GGG GAC ACA TGG AAC	594
	360	Met Val Ala Leu Gly Ile Phe Gly Lys Lys Cys Tyr Leu Gly Asp Thr Trp Asn	
	361		
	362		
	363	CGC CTG GAT TTC TTC ATC GTC ATG GCA GGC AAC ATC AAC CTG TCA GCC ATC CGC	648
	364	Arg Leu Asp Phe Phe Ile Val Met Ala Gly Asn Ile Asn Leu Ser Ala Ile Arg	
	365		
	366		
	367	ACC GTG CGC GTC CTG AGG CCC CTC AAA GCC ATC AAC CGC GTG CCC AGT ATG CGG	702
	368	Thr Val Arg Val Leu Arg Pro Leu Lys Ala Ile Asn Arg Val Pro Ser Met Arg	
	369		
	370		
	371	ATC CTG GTG AAC CTG CTC CTG GAC ACA CTG CCC ATG CTG GGG AAT GTC CTG CTG	756
	372	Ile Leu Val Asn Leu Leu Leu Asp Thr Leu Pro Met Leu Gly Asn Val Leu Leu	
	373		
	374		
	375	CTC TGC TTC TTT GTC TTC TTC ATC TTT GGC ATC ATA GGT GTG CAG CTC TGG GCG	810
	376	Leu Cys Phe Phe Val Phe Phe Ile Phe Gly Ile Ile Gly Val Gln Leu Trp Ala	
	377		
	378		
	379	GGC CTG CTG CGT AAC CGC TGC TTC CTG GAG GAG AAC TTC ACC ATA CAA GGG GAT	864
	380	Gly Leu Leu Arg Asn Arg Cys Phe Leu Glu Glu Asn Phe Thr Ile Gln Gly Asp	
	381		
	382		
	383	GTG GCC TTG CCC CCA TAC TAC CAG CCG GAG GAG GAT GAT GAG ATG CCC TTC ATC	918

Number amino acids throughout

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384	Val	Ala	Leu	Pro	Pro	Tyr	Tyr	Gln	Pro	Glu	Glu	Asp	Asp	Glu	Met	Pro	Phe	Ile	
385																			
386																			
387	TGC	TCC	CTG	TCG	GGC	GAC	AAT	GGG	ATA	ATG	GGC	TGC	CAT	GAG	ATC	CCC	CCG	CTC	972
388	Cys	Ser	Leu	Ser	Gly	Asp	Asn	Gly	Ile	Met	Gly	Cys	His	Glu	Ile	Pro	Pro	Leu	
389																			
390																			
391	AAG	GAG	CAG	GGC	CGT	GAG	TGC	TGC	CTG	TCC	AAG	GAC	GAC	GTC	TAC	GAC	TTT	GGG	1026
392	Lys	Glu	Gln	Gly	Arg	Glu	Cys	Cys	Leu	Ser	Lys	Asp	Asp	Val	Tyr	Asp	Phe	Gly	
393																			
394																			
395	GCG	GGG	CGC	CAG	GAC	CTC	AAT	GCC	AGC	GGC	CTC	TGT	GTC	AAC	TGG	AAC	CGT	TAC	1080
396	Ala	Gly	Arg	Gln	Asp	Leu	Asn	Ala	Ser	Gly	Leu	Cys	Val	Asn	Trp	Asn	Arg	Tyr	
397																			
398																			
399																			
400	TAC	AAT	GTG	TGC	CGC	ACG	GGC	AGC	GCC	AAC	CCC	CAC	AAG	GGT	GCC	ATC	AAC	TTT	1134
401	Tyr	Asn	Val	Cys	Arg	Thr	Gly	Ser	Ala	Asn	Pro	His	Lys	Gly	Ala	Ile	Asn	Phe	
402																			
403																			
404	GAC	AAC	ATC	GGT	TAT	GCT	TGG	ATT	GTC	ATC	TTC	CAG	GTG	ATC	ACT	CTG	GAA	GGC	1188
405	Asp	Asn	Ile	Gly	Tyr	Ala	Trp	Ile	Val	Ile	Phe	Gln	Val	Ile	Thr	Leu	Glu	Gly	
406																			
407																			
408	TGG	GTG	GAG	ATC	ATG	TAC	TAC	GTG	ATG	GAT	GCT	CAC	TCC	TTC	TAC	AAC	TTC	ATC	1242
409	Trp	Val	Glu	Ile	Met	Tyr	Tyr	Val	Met	Asp	Ala	His	Ser	Phe	Tyr	Asn	Phe	Ile	
410																			
411																			
412	TAC	TTC	ATC	CTG	CTT	ATC	ATA	AGT	GAG	CTC	ATC	CAC	CTC	GTC	ATG	CCT	GAC	TGC	1296
413	Tyr	Phe	Ile	Leu	Leu	Ile	Ile	Ser	Glu	Leu	Ile	His	Leu	Val	Met	Pro	Asp	Cys	
414																			
415																			
416	AGC	TTC	AGC	ACA	GCA	CAG	TCC	CCA	AAA	TGT	CAA	GGT	GAT	TCA	CTC	CCA	GGA	GTC	1350
417	Ser	Phe	Ser	Thr	Ala	Gln	Ser	Pro	Lys	Cys	Gln	Gly	Asp	Ser	Leu	Pro	Gly	Val	
418																			
419																			
420	GCT	GCT	GAA	TCC	CTG	CTG	CTG	CGA	GAC	TCT	AGC	TCC	TCA	GTC	ATC	ACT	GAT	GAG	1404
421	Ala	Ala	Glu	Ser	Leu	Leu	Leu	Arg	Asp	Ser	Ser	Ser	Ser	Val	Ile	Thr	Asp	Glu	
422																			
423																			
424	GCT	GCA	GCC	ATG	GAG	AAC	CTC	CTG	GCG	GGC	ACC	TCC	AAG	GGG	GAT	GAA	AGC	TAT	1458
425	Ala	Ala	Ala	Met	Glu	Asn	Leu	Leu	Ala	Gly	Thr	Ser	Lys	Gly	Asp	Glu	Ser	Tyr	
426																			
427																			
428	CTG	CTC	AGG	CTG	GCC	GGC	AGC	CAA	GTT	CAC	TCC	CAG	GCT	CAG	CAA	ATG	CTG	GGG	1512
429	Leu	Leu	Arg	Leu	Ala	Gly	Ser	Gln	Val	His	Ser	Gln	Ala	Gln	Gln	Met	Leu	Gly	
430																			
431																			
432	AGG	GGG	CTG	GGC	CCT	GAA	AGC	CTG	GAA	ACT	GGA	GAG	GAG	CCC	CAC	TCG	TGG	AGC	1566
433	Arg	Gly	Leu	Gly	Pro	Glu	Ser	Leu	Glu	Thr	Gly	Glu	Glu	Pro	His	Ser	Trp	Ser	
434																			
435																			
436	CCT	CGG	GCC	ACA	AGG	AGA	TGG	GAT	CCC	CAA	TGC	CAA	CCA	GGG	CAG	CCT	CTC	CCC	1620

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437	Pro Arg Ala Thr Arg Arg Trp Asp Pro Gln Cys Gln Pro Gly Gln Pro Leu Pro	
438		
439		
440	CTT CAT TTC ATG CAA GCA CAG GTG GGC TCC TTC TTC ATG ATC AAC CTG TGC CTC	1674
441	Leu His Phe Met Gln Ala Gln Val Gly Ser Phe Phe Met Ile Asn Leu Cys Leu	
442		
443		
444	GTT GTC ATA GCG ACC CAG TTC TCG GAG ACC AAG CAA CGG GAG CAC CGG CTG ATG	1728
445	Val Val Ile Ala Thr Gln Phe Ser Glu Thr Lys Gln Arg Glu His Arg Leu Met	
446		
447		
448	CTG GAG CAG CGG CAG CGC TAC CTG TCC TCC AGC ACG GTG GCC AGC TAC GCC GAG	1782
449	Leu Glu Gln Arg Gln Arg Tyr Leu Ser Ser Ser Thr Val Ala Ser Tyr Ala Glu	
450		
451		
452	CCT GGC GAC TGC TAC GAG GAG ATC TTC CAG TAT GTC TGC CAC ATC CTG CGC AAG	1836
453	Pro Gly Asp Cys Tyr Glu Glu Ile Phe Gln Tyr Val Cys His Ile Leu Arg Lys	
454		
455		
456		
457	GCC AAG CGC CGC GCC CTG GGC CTC TAC CAG GCC CTG CAG AGC CGG CGC CAG GCC	1890
458	Ala Lys Arg Arg Ala Leu Gly Leu Tyr Gln Ala Leu Gln Ser Arg Arg Gln Ala	
459		
460		
461	CTG GGC CCG GAG GCC CCG GCC CCC GCC AAA CCT GGG CCC CAC GCC AAG GAG CCC	1944
462	Leu Gly Pro Glu Ala Pro Ala Pro Ala Lys Pro Gly Pro His Ala Lys Glu Pro	
463		
464		
465	CGG CAC TAC CCT CTC ACA GTC TGG GAA TCG ATT CTT GGG AGG CAA GCA GAA GAA	1998
466	Arg His Tyr Pro Leu Thr Val Trp Glu Ser Ile Leu Gly Arg Gln Ala Glu Glu	
467		
468		
--> 469	TGC ACG CTC AGA GCT GCC GCC CAC CCG TCC TCG GGT GCC AGC CAT CCA GGC GTG	2049 2052
470	Cys Thr Leu Arg Ala Ala Ala His Pro Ser Ser Gly Ala Ser His Pro Gly Val	
471		
472		
--> 473	GGC TCG GAG GAG GCC CCA GAG CTG TGC CCG CAA CAT AGC CCC CTG GAT GCG ACG	2106 O/K
474	Gly Ser Glu Glu Ala Pro Glu Leu Cys Pro Gln His Ser Pro Leu Asp Ala Thr	
475		
476		
477	CCC CAC ACC CTG GTG CAG CCC ATC CCC GCC ACG CTG GCT TCC GAT CCC GCC AGC	2160
478	Pro His Thr Leu Val Gln Pro Ile Pro Ala Thr Leu Ala Ser Asp Pro Ala Ser	
479		
480		
481	TGC CCT TGC TGC CAG CAT GAG GAC GGC CGG CGG CCC TCG GGC CTG GGC AGC ACC	2214
482	Cys Pro Cys Cys Gln His Glu Asp Gly Arg Arg Pro Ser Gly Leu Gly Ser Thr	
483		
484		
485	GAC TCG GGC CAG GAG GGC TCG GGC TCC GGG AGC TCC GCT GGT GGC GAG GAC GAG	2268
486	Asp Ser Gly Gln Glu Gly Ser Gly Ser Gly Ser Ser Ala Gly Gly Glu Asp Glu	
487		
488		
489	GCG GAT GGG GAC GGG GCC CGG AGC AGC GAG GAC GGA GCC TCC TCA GAA CTG GGG	2322

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INPUT SET: S2880.raw

490	Ala Asp Gly Asp Gly Ala Arg Ser Ser Glu Asp Gly Ala Ser Ser Glu Leu Gly	
491		
492		
493	AAG GAG GAG GAG GAG GAG GAG CAG GCG GAT GGG GCG GTC TGG CTG TGC GGG GAT	2376
494	Lys Glu Glu Glu Glu Glu Glu Gln Ala Asp Gly Ala Val Trp Leu Cys Gly Asp	
495		
496		
497	GTG TGG CGG GAG ACG CGA GCC AAG CTG CGC GGC ATC GTG GAC AGC AAG TAC TTC	2430
498	Val Trp Arg Glu Thr Arg Ala Lys Leu Arg Gly Ile Val Asp Ser Lys Tyr Phe	
499		
500		
501	AAC CGG GGC ATC ATG ATG GCC ATC CTG GTC AAC ACC GTC AGC ATG GGC ATC GAG	2484
502	Asn Arg Gly Ile Met Met Ala Ile Leu Val Asn Thr Val Ser Met Gly Ile Glu	
503		
504		
505	CAC CAC GAG CAG GCC AGT GCA GCG CAG CCG GGC CGG GCC TGC GGG AGA GGA CAA	2538
506	His His Glu Gln Ala Ser Ala Ala Gln Pro Gly Arg Ala Cys Gly Arg Gly Gln	
507		
508		
509	AAT CCA GAC CTT TGC ATG ACC CTC AAG GCC CCT TGT CTC TGT CAC AAC GTC CCT	2592
510	Asn Pro Asp Leu Cys Met Thr Leu Lys Ala Pro Cys Leu Cys His Asn Val Pro	
511		
512		
513		
514	TCA CCA GGC CAG GGT GTC CTG TCC CAT CCA GTG ACT CCA CCC CAT ACA GCC CCA	2646
515	Ser Pro Gly Gln Gly Val Leu Ser His Pro Val Thr Pro Pro His Thr Ala Pro	
516		
517		
518	TGG CGC ATG GAG ACA GGA AAG CAG GGA CAC GGA TGT GAA GAA GGA CCA GGA CAA	2700
519	Trp Arg Met Glu Thr Gly Lys Gln Gly His Gly Cys Glu Glu Gly Pro Gly Gln	
520		
521		
522	CGA AGC AGT GAC ATG TTT GCC CTG GAG ATG ATC CTG AAG CTG GCT GCA TTT GGG	2754
523	Arg Ser Ser Asp Met Phe Ala Leu Glu Met Ile Leu Lys Leu Ala Ala Phe Gly	
524		
525		
526	CTC TTC GAC TAC CTG CGT AAC CCC TAC AAC ATC TTC GAC AGC ATC ATT GTC ATC	2808
527	Leu Phe Asp Tyr Leu Arg Asn Pro Tyr Asn Ile Phe Asp Ser Ile Ile Val Ile	
528		
529		
530	ATC AGC ATC TGG GAG ATC GTG GGG CAG GCG GAC GGT GGG CTG TCG GTG CTG CGG	2862
531	Ile Ser Ile Trp Glu Ile Val Gly Gln Ala Asp Gly Gly Leu Ser Val Leu Arg	
532		
533		
534	ACC TTC CGG CTG CTG CGC GTG CTG AAA CTG GTG CGC TTC ATG CCT GCC CTG CGG	2916
535	Thr Phe Arg Leu Leu Arg Val Leu Lys Leu Val Arg Phe Met Pro Ala Leu Arg	
536		
537		
538	CGC CAG CTC GTG GTG CTC ATG AAG ACC ATG GAC AAC GTG GCC ACC TTC TGC ATG	2970
539	Arg Gln Leu Val Val Leu Met Lys Thr Met Asp Asn Val Ala Thr Phe Cys Met	
540		
541		
542	CTG CTC ATG CTC TTC ATC TTC ATC TTC AGC ATC CTT GGG ATG CAT ATT TTT GGC	3024

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543	Leu Leu Met Leu Phe Ile Phe Ile Phe Ser Ile Leu Gly Met His Ile Phe Gly	
544		
545		
546	TGC AAG TTC AGC CTC CGC ACG GAC ACT GGA GAC ACG GTG CCC GAC AGG AAG AAC	3078
547	Cys Lys Phe Ser Leu Arg Thr Asp Thr Gly Asp Thr Val Pro Asp Arg Lys Asn	
548		
549		
550	TTC GAC TCC CTG CTG TGG GCC ATC GTC ACT GTG TTC CAG ATC CTC ACC CAG GAG	3132
551	Phe Asp Ser Leu Leu Trp Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu	
552		
553		
554	GAC TGG AAC GTC GTT CTC TAC AAT GGC ATG GCC TCC ACT TCT CCC TGG GCC TCC	3186
555	Asp Trp Asn Val Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Pro Trp Ala Ser	
556		
557		
558	CTC TAC TTT GTC GCC CTC ATG ACC TTC GGC AAC TAT GTG CTC TTC AAC CTG CTG	3240
559	Leu Tyr Phe Val Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu	
560		
561		
562	GTG GCC ATC CTG GTG GAG GGC TTC CAG GCG GAG GTG ACT GTG GTC TTG GCA GAG	3294
563	Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Val Thr Val Val Leu Ala Glu	
564		
565		
566	GAA GCA CCC CCA CAG GGC CTG CGA AAG ACT GGG CGA GGG AGA GGT GGC CTG GAT	3348
567	Glu Ala Pro Pro Gln Gly Leu Arg Lys Thr Gly Arg Gly Arg Gly Gly Leu Asp	
568		
569		
570		
571	GGG GGA GGG CTG CAA TTC AAA CTT CTA GCA GGC AAC CTA TCC CTA AAG GAG GGG	3402
572	Gly Gly Gly Leu Gln Phe Lys Leu Leu Ala Gly Asn Leu Ser Leu Lys Glu Gly	
573		
574		
575	GTT GCT GAT GAG GTG GGT GAC GCC AAT CGC TCC TAC TCG GAC GAG GAC CAG AGC	3456
576	Val Ala Asp Glu Val Gly Asp Ala Asn Arg Ser Tyr Ser Asp Glu Asp Gln Ser	
577		
578		
579	TCA TCC AAC ATA GAA GAG TTT GAT AAG CTC CAG GAA GGC CTG GAC AGC AGC GGA	3510
580	Ser Ser Asn Ile Glu Glu Phe Asp Lys Leu Gln Glu Gly Leu Asp Ser Ser Gly	
581		
582		
583	GAT CCC AAG CTC TGC CCA ATC CCC ATG ACC CCC AAT GGG CAC CTG GAC CCC AGT	3564
584	Asp Pro Lys Leu Cys Pro Ile Pro Met Thr Pro Asn Gly His Leu Asp Pro Ser	
585		
586		
587	CTC CCA CTG GGT GGG CAC CTA GGT CCT GCT GGG GCT GCG GGA CCT GCC CCC CGA	3618
588	Leu Pro Leu Gly Gly His Leu Gly Pro Ala Gly Ala Ala Gly Pro Ala Pro Arg	
589		
590		
591	CTC TCA CTG CAG CCG GAC CCC ATG CTG GTG GCC CTG GGC TCC CGA AAG AGC AGC	3672
592	Leu Ser Leu Gln Pro Asp Pro Met Leu Val Ala Leu Gly Ser Arg Lys Ser Ser	
593		
594		
595	GTC ATG TCT CTA GGG AGG ATG AGC TAT GAC CAG CGC TCC CTG GTG GGT GGT CTT	3726

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INPUT SET: S2880.raw

596	Val Met Ser Leu Gly Arg Met Ser Tyr Asp Gln Arg Ser Leu Val Gly Gly Leu	
597		
598		
599	AGA GCC ACA GCG GGG GTG CAG GCT GCC TTT GGG CAC CTG GTG CCC CAG CCG TGG	3780
600	Arg Ala Thr Ala Gly Val Gln Ala Ala Phe Gly His Leu Val Pro Gln Pro Trp	
601		
602		
603	GTG TGC CTG TGG GGC GCT GAC CCG AAC GGG AAC TCC TTC CAG TCC AGC TCC CGG	3834
604	Val Cys Leu Trp Gly Ala Asp Pro Asn Gly Asn Ser Phe Gln Ser Ser Ser Arg	
605		
606		
607	AGC TCC TAC TAC GGG CCA TGG GGC CGC AGC GCG GCC TGG GCC AGC CGT CGC TCC	3888
608	Ser Ser Tyr Tyr Gly Pro Trp Gly Arg Ser Ala Ala Trp Ala Ser Arg Arg Ser	
609		
610		
611	AGC TGG AAC AGC CTC AAG CAC AAG CCG CCG TCG GCG GAG CAT GAG TCC CTG CTC	3942
612	Ser Trp Asn Ser Leu Lys His Lys Pro Pro Ser Ala Glu His Glu Ser Leu Leu	
613		
614		
615	TCT GCG GAG CGC GGC GGC GGC GCC CGG GTC TGC GAG GTT GCC GCG GAC GAG GGG	3996
616	Ser Ala Glu Arg Gly Gly Gly Ala Arg Val Cys Glu Val Ala Ala Asp Glu Gly	
617		
618		
619	CCG CCG CGG GCC GCA CCC CTG CAC ACC CCA CAC GCC CAC CAC GTT CAT CAC GGG	4050
620	Pro Pro Arg Ala Ala Pro Leu His Thr Pro His Ala His His Val His His Gly	
621		
622		
623	CCC CAT CTG GCG CAC CGC CAC CGC CAC CAC CGC CGG ACG CTG TCC CTC GAC AAC	4104
624	Pro His Leu Ala His Arg His Arg His His Arg Arg Thr Leu Ser Leu Asp Asn	
625		
626		
627		
628	AGG GAC TCG GTG GAC CTG GCC GAG CTG GTG CCC GCG GTG GGC GCC CAC CCC CGG	4158
629	Arg Asp Ser Val Asp Leu Ala Glu Leu Val Pro Ala Val Gly Ala His Pro Arg	
630		
631		
632	GCC GCC TGG AGG GCG GCA GGC CCG GCC CCC GGG CAT GAG GAC TGC AAT GGC AGG	4212
633	Ala Ala Trp Arg Ala Ala Gly Pro Ala Pro Gly His Glu Asp Cys Asn Gly Arg	
634		
635		
636	ATG CCC AGC ATC GCC AAA GAC GTC TTC ACC AAG ATG GGC GAC CGC GGG GAT CGC	4266
637	Met Pro Ser Ile Ala Lys Asp Val Phe Thr Lys Met Gly Asp Arg Gly Asp Arg	
638		
639		
640	GGG GAG GAT GAG GAG GAA ATC GAC TAC GTG AGT GGG GGC GGG GCC GAA GGG GAC	4320
641	Gly Glu Asp Glu Glu Glu Ile Asp Tyr Val Ser Gly Gly Gly Ala Glu Gly Asp	
642		
643		
644	CTG ACC CTG TGC TTC CGC GTC CGC AAG ATG ATC GAC GTC TAT AAG CCC GAC TGG	4374
645	Leu Thr Leu Cys Phe Arg Val Arg Lys Met Ile Asp Val Tyr Lys Pro Asp Trp	
646		
647		
648	TGC GAG GTC CGC GAA GAC TGG TCT GTC TAC CTC TTC TCT CCC GAG AAC AGG CTC	4428

RAW SEQUENCE LISTING PATENT APPLICATION US/09/030,482

DATE: 03/07/98
TIME: 13:54:24

INPUT SET: S2880.raw

649	Cys Glu Val Arg Glu Asp Trp Ser Val Tyr Leu Phe Ser Pro Glu Asn Arg Leu	
650		
651		
652	AGG GAT CTG GGC TGG GTA AGC CTC GAG TGC CAG GGA AAG GTG GGT GAC CTC GTG	4482
653	Arg Asp Leu Gly Trp Val Ser Leu Glu Cys Gln Gly Lys Val Gly Asp Leu Val	
654		
655		
656	GTG TGG GTG TAT GGT CAG AGG AGG CAG CGC CAG ACC ATT ATT GCC CAC AAA CTC	4536
657	Val Trp Val Tyr Gly Gln Arg Arg Gln Arg Gln Thr Ile Ile Ala His Lys Leu	
658		
659		
660	TTC GAC TAC GTC GTC CTG GCC TTC ATC TTT CTC AAC TGC ATC ACC ATC GCC CTG	4590
661	Phe Asp Tyr Val Val Leu Ala Phe Ile Phe Leu Asn Cys Ile Thr Ile Ala Leu	
662		
663		
664	GAG CGG CCT CAG ATC GAG GCC GGC AGC ACC GAA CGC ATC TTT CTC ACC GTG TCC	4644
665	Glu Arg Pro Gln Ile Glu Ala Gly Ser Thr Glu Arg Ile Phe Leu Thr Val Ser	
666		
667		
668	AAC TAC ATC TTC ACG GCC ATC TTC GTG GGC GAG ATG ACA TTG AAG GTA GTC TCG	4698
669	Asn Tyr Ile Phe Thr Ala Ile Phe Val Gly Glu Met Thr Leu Lys Val Val Ser	
670		
671		
672	CTG GGC CTG TAC TTC GGC GAG CAG GCG TAC CTA CGC AGC AGC TGG AAC GTG CTG	4752
673	Leu Gly Leu Tyr Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu	
674		
675		
676	GAT GGC TTT CTT GTC TTC GTG TCC ATC ATC GAC ATC GTG GTG TCC CTG GCC TCA	4806
677	Asp Gly Phe Leu Val Phe Val Ser Ile Ile Asp Ile Val Val Ser Leu Ala Ser	
678		
679		
680	GCC GGG GGA GCC AAG ATC TTG GGG GTC CTC CGA GTC TTG CGG CTC CTG CGC ACC	4860
681	Ala Gly Gly Ala Lys Ile Leu Gly Val Leu Arg Val Leu Arg Leu Leu Arg Thr	
682		
683		
684		
685	CTA CGC CCC CTG CGT GTC ATC AGC CGG GCG CCG GGC CTG AAG CTG GTG GTG GAG	4914
686	Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Pro Gly Leu Lys Leu Val Val Glu	
687		
688		
689	ACA CTC ATC TCC TCC CTC AAG CCC ATC GGC AAC ATC GTG CTC ATC TGC TGT GCC	4968
690	Thr Leu Ile Ser Ser Leu Lys Pro Ile Gly Asn Ile Val Leu Ile Cys Cys Ala	
691		
692		
693	TTC TTC ATC ATC TTT GGC ATC CTG GGA GTG CAG CTC TTC AAG GGC AAG TTC TAC	5022
694	Phe Phe Ile Ile Phe Gly Ile Leu Gly Val Gln Leu Phe Lys Gly Lys Phe Tyr	
695		
696		
697	CAC TGT CTG GGC GTG GAC ACC CGC AAC ATC ACC AAC CGC TCG GAC TGC ATG GCC	5076
698	His Cys Leu Gly Val Asp Thr Arg Asn Ile Thr Asn Arg Ser Asp Cys Met Ala	
699		
700		
701	GCC AAC TAC CGC TGG GTC CAT CAC AAA TAC AAC TTC GAC AAC CTG GGC CAG GCT	5130

RAW SEQUENCE LISTING PATENT APPLICATION US/09/030,482

DATE: 03/07/98
TIME: 13:54:30

INPUT SET: S2880.raw

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702  Ala Asn Tyr Arg Trp Val His His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala
703
704
--> 705  CTG ATG TCC CTC TTT GTC CTG GCA TCC AAG GAT GGT TGG GTG AAC ATC ATG TAC 5185 5184
706  Leu Met Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asn Ile Met Tyr
707
708
--> 709  AAT GGA CTG GAT GCT GTT GCT GTG GAC CAG CAG CCT GTG ACC AAC CAC AAC CCC 5238 OK
710  Asn Gly Leu Asp Ala Val Ala Val Asp Gln Gln Pro Val Thr Asn His Asn Pro
711
712
713  TGG ATG CTG CTG TAC TTC ATC TCC TTC CTG CTC ATC GTC AGC TTC TTT GTG CTC 5292
714  Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ser Phe Phe Val Leu
715
716
717  AAC ATG TTT GTG GGT GTC GTG GTG GAG AAC TTC CAC AAG TGC CGG CAG CAC CAG 5346
718  Asn Met Phe Val Gly Val Val Val Glu Asn Phe His Lys Cys Arg Gln His Gln
719
720
721  GAG GCT GAA GAG GCA CGG CGG CGT GAG GAG AAG CGG CTG CGG CGC CTG GAG AAG 5400
722  Glu Ala Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg Leu Arg Arg Leu Glu Lys
723
724
725  AAG CGC CGG AAG GCC CAG CGG CTG CCC TAC TAT GCC ACC TAT TGT CAC ACC CGG 5454
726  Lys Arg Arg Lys Ala Gln Arg Leu Pro Tyr Tyr Ala Thr Tyr Cys His Thr Arg
727
728
729  CTG CTC ATC CAC TCC ATG TGC ACC AGC CAC TAC CTG GAC ATC TTC ATC ACC TTC 5508
730  Leu Leu Ile His Ser Met Cys Thr Ser His Tyr Leu Asp Ile Phe Ile Thr Phe
731
732
733  ATC ATC TGC CTC AAC GTG GTC ACC ATG TCC CTG GAG CAC TAC AAT CAG CCC ACG 5562
734  Ile Ile Cys Leu Asn Val Val Thr Met Ser Leu Glu His Tyr Asn Gln Pro Thr
735
736

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/030,482DATE: 03/07/98
TIME: 13:54:37*INPUT SET: S2880.raw*

Line	Error	Original Text
107	# of Sequences for line conflicts w/ running total	GTAAATCCA ACGTCTTCTA CTGG 28
269	Entered (123) and Calc. Seq. Length (120) differ	(A) LENGTH: 123
331	# of Sequences for line conflicts w/ running total	ATG TTC AAA TTG GTG GCC ACT GTT GCT CGA AC
335	# of Sequences for line conflicts w/ running total	ACG GGT GGT CCT GGA ACA GGG ATG CAC ACG G
469	# of Sequences for line conflicts w/ running total	TGC ACG CTC AGA GCT GCC GCC CAC CCG TCC TC
473	# of Sequences for line conflicts w/ running total	GGC TCG GAG GAG GCC CCA GAG CTG TGC CCG CA
705	# of Sequences for line conflicts w/ running total	CTG ATG TCC CTC TTT GTC CTG GCA TCC AAG GA
709	# of Sequences for line conflicts w/ running total	AAT GGA CTG GAT GCT GTT GCT GTG GAC CAG CA